

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBY26, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISSUES

<130> D0128NP

<150> US 60/273,963

<151> 2001-03-07

<150> US 60/278,927

<151> 2001-03-27

<160> 76

<170> PatentIn version 3.0

<210> 1

<211> 2260

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (440)..(1444)

<400> 1

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cagcgtgagg tgagagaatgg gttctaaact gaatgacagc tgttaacagt ttttggccct      180
gtttttcctg tcctgaatcc tcaactgaga tcctagggat gagaaacggg ggaacagcac      240
gccctacttg agagaattag aatttgaggc gctaggaagc aaaggatgcc caaagatggc      300
gacctgccag cctggactgc cagcgaaggc cagaatcgtg ctgtagctct gaaccacag      360
ctcctctgcc cctggcccat gagaatttca gctggagaga tagcatgcc tggtaaagtga      420
agtccctgcca cttcgagac atg gaa tca tct ttc tca ttt gga gtg atc ctt      472
          Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu
          1                      5                      10

gct gtc ctg gcc tcc ctg atc att gct act aac aca cta gtg gct gtg      520
Ala Val Leu Ala Ser Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val
          15                      20                      25

gct gtg ctg ctg ttg atc cac aag aat gat ggt gtc agt ctc tgc ttc      568
Ala Val Leu Leu Leu Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe
          30                      35                      40

acc ttg aat ctg gct gtg gct gac acc ttg att ggt gtg gcc atc tct      616
Thr Leu Asn Leu Ala Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser

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45	50	55	
ggc cta ctc aca gac cag ctc tcc agc cct tct cgg ccc aca cag aag Gly Leu Leu Thr Asp Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys 60 65 70 75			664
acc ctg tgc agc ctg cgg atg gca ttt gtc act tcc tcc gca gct gcc Thr Leu Cys Ser Leu Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala 80 85 90			712
tct gtc ctc acg gtc atg ctg atc acc ttt gac agg tac ctt gcc atc Ser Val Leu Thr Val Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile 95 100 105			760
aag cag ccc ttc cgc tac ttg aag atc atg agt ggg ttc gtg gcc ggg Lys Gln Pro Phe Arg Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly 110 115 120			808
gcc tgc att gcc ggg ctg tgg tta gtg tct tac ctc att ggc ttc ctc Ala Cys Ile Ala Gly Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu 125 130 135			856
cca ctc gga atc ccc atg ttc cag cag act gcc tac aaa ggg cag tgc Pro Leu Gly Ile Pro Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys 140 145 150 155			904
agc ttc ttt gct gta ttt cac cct cac ttc gtg ctg acc ctc tcc tgc Ser Phe Phe Ala Val Phe His Pro His Phe Val Leu Thr Leu Ser Cys 160 165 170			952
gtt ggc ttc ttc cca gcc atg ctc ctc ttt gtc ttc ttc tac tgc gac Val Gly Phe Phe Pro Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp 175 180 185			1000
atg ctc aag att gcc tcc atg cac agc cag cag att cga aag atg gaa Met Leu Lys Ile Ala Ser Met His Ser Gln Gln Ile Arg Lys Met Glu 190 195 200			1048
cat gca gga gcc atg gct gga ggt tat cga tcc cca cgg act ccc agc His Ala Gly Ala Met Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser 205 210 215			1096
gac ttc aaa gct ctc cgt act gtg tct gtt ctc att ggg agc ttt gct Asp Phe Lys Ala Leu Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala 220 225 230 235			1144
cta tcc tgg acc ccc ttc ctt atc act ggc att gtg cag gtg gcc tgc Leu Ser Trp Thr Pro Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys 240 245 250			1192
cag gag tgt cac ctc tac cta gtg ctg gaa cgg tac ctg tgg ctg ctc Gln Glu Cys His Leu Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu 255 260 265			1240
ggc gtg ggc aac tcc ctg ctc aac cca ctc atc tat gcc tat tgg cag Gly Val Gly Asn Ser Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln 270 275 280			1288

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aag gag gtg cga ctg cag ctc tac cac atg gcc cta gga gtg aag aag      1336
Lys Glu Val Arg Leu Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys
    285                      290                      295

gtg ctc acc tca ttc ctc ctc ttt ctc tcg gcc agg aat tgt ggc cca      1384
Val Leu Thr Ser Phe Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro
    300                      305                      310                      315

gag agg ccc agg gaa agt tcc tgt cac atc gtc act atc tcc agc tca      1432
Glu Arg Pro Arg Glu Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser
    320                      325                      330

gag ttt gat ggc taagacgtcg ctttgcttac cagtctggcc cagaggagaa      1484
Glu Phe Asp Gly
    335

acatgcttcg ttccaccata gcaagcatcg tgctcctaca actgaagaac tttttgactc      1544

tcaagtggac gatggaaccc aatatgcctt gaaatgctga gcattccagca agtaccaggc      1604

cagcaataag gcacattctt ggattgtatt gtgagttact gggaactagg taaaatacga      1664

ataactggat ttggacaaa attgaaagca ggctcaaacc aatgccctcc ttactggtgg      1724

ttcaaaagctt aaatcctggc ctgtctacaa aggactgac ttgccaagat aatataagca      1784

aagtggaatg aaaattaaag ttaattctga agccaaggtc cttttagaaa aaaaaaagta      1844

aattagcctg atttaatcat tccacatttt aaacatatat caacatcaca ttgtacccca      1904

cgtaatatat acaattatttt gtcaattaaa aataaaaaat atatatTTTT aagtacagaa      1964

aagcaggagg ggaggagagg ccagggtgac agtgtgttat taggttcaat ctaagaaact      2024

ctgtactccc tgggagtcag tatgtgcaat ggaaaaatca caggctctga aatccaacag      2084

accagtgctc aaatgataat tcagtcattt aaattctcaa actagatctc gcattcatca      2144

aaccgggcta ataatgccta ctttacatgg ttatattgaa gattaactca gataatgtat      2204

atgtaaatat ctagtaaact acagcacatt gttagtgtct aaaaaaaaaa aaaaag      2260

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<210> 2
<211> 335
<212> PRT
<213> homo sapiens

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<400> 2
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Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
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Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
20          25          30

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Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 100 105 110
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
 145 150 155 160
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
 165 170 175
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
 180 185 190
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
 195 200 205
 Ala Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
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Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
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<210> 3

<211> 388

<212> PRT

<213> CAVIA PORCELLUS

<400> 3

Met Asp Lys Leu Asp Ala Asn Val Ser Ser Lys Glu Gly Phe Gly Ser
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Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Ala Val Ile Leu Met
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Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Arg Asp Arg
35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
65 70 75 80

Leu Val Gln Asp Ile Trp Val Tyr Gly Glu Met Phe Cys Leu Val Arg
85 90 95

Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys
100 105 110

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
115 120 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
130 135 140

Cys Trp Val Ile Pro Met Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145 150 155 160

Trp Asn Asn Ile Gly Ile Val Asp Leu Ile Glu Lys Arg Lys Phe Asn
165 170 175

Gln Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr
180 185 190

Ala Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met
195 200 205

Val Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala Arg
210 215 220

Gln Ile Gln Val Leu Gln Arg Ala Gly Ala Pro Ala Glu Gly Arg Pro
225 230 235 240

Gln Pro Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys
245 250 255

Ala Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp
260 265 270

Ala Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr
275 280 285

Val Pro Gly Gln Leu Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn
290 295 300

Ser Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg
305 310 315 320

Arg Ala Phe Leu Ile Ile Leu Cys Cys Asp Glu Arg Tyr Arg Arg
325 330 335

Pro Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn
340 345 350

Gly Ser Thr His Val Leu Arg Asp Thr Val Glu Cys Gly Gly Gln Trp
355 360 365

Glu Ser Gln Cys His Pro Ala Ala Ser Ser Pro Leu Val Ala Ala Gln
370 375 380

Pro Ile Asp Thr
385

<210> 4

<211> 391

<212> PRT

<213> BRANCHIOSTOMA LANCEOLATUM

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Pro	Tyr	Ser	Ala	Gly	Val	Gln	Ala	Val	Leu	Gly	Leu	Ile	Thr	Val	Ile						
		35					40					45									
Leu	Ile	Leu	Leu	Thr	Val	Ile	Gly	Asn	Val	Leu	Val	Ile	Leu	Ala	Val						
	50					55					60										
Thr	Cys	His	Arg	Lys	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Val	Ser						
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Leu	Ala	Cys	Ala	Asp	Leu	Ser	Val	Gly	Ile	Thr	Val	Leu	Pro	Phe	Ala						
				85					90					95							
Ala	Thr	Asn	Asp	Ile	Leu	Gly	Tyr	Trp	Pro	Phe	Gly	Gly	Tyr	Cys	Asp						
			100					105					110								
Val	Trp	Val	Ser	Phe	Asp	Val	Leu	Asn	Ser	Thr	Ala	Ser	Ile	Leu	Asn						
		115					120					125									
Leu	Val	Val	Ile	Ala	Phe	Asp	Arg	Phe	Leu	Ala	Ile	Thr	Ala	Pro	Phe						
	130					135					140										
Thr	Tyr	His	Thr	Arg	Met	Thr	Glu	Arg	Thr	Ala	Gly	Ile	Leu	Ile	Ala						
145					150					155					160						
Thr	Val	Trp	Gly	Ile	Ser	Leu	Val	Val	Ser	Phe	Leu	Pro	Ile	Gln	Ala						
				165					170					175							
Gly	Trp	Tyr	Arg	Asp	Asn	Gln	Ser	Glu	Glu	Ala	Leu	Ala	Ile	Tyr	Ser						
			180					185					190								
Asp	Pro	Cys	Leu	Cys	Ile	Phe	Thr	Ala	Ser	Thr	Ala	Tyr	Thr	Ile	Val						
		195					200					205									
Ser	Ser	Leu	Ile	Ser	Phe	Tyr	Ile	Pro	Leu	Leu	Ile	Met	Leu	Val	Phe						
	210					215					220										
Tyr	Gly	Ile	Ile	Phe	Lys	Ala	Ala	Arg	Asp	Gln	Ala	Arg	Lys	Ile	Asn						
225					230					235					240						
Ala	Leu	Glu	Gly	Arg	Leu	Glu	Gln	Glu	Asn	Asn	Arg	Gly	Lys	Lys	Ile						
				245					250					255							
Ser	Leu	Ala	Lys	Glu	Lys	Lys	Ala	Ala	Lys	Thr	Leu	Gly	Ile	Ile	Met						
			260					265					270								
Gly	Val	Phe	Ile	Leu	Cys	Trp	Leu	Pro	Phe	Phe	Val	Val	Asn	Ile	Val						
		275					280					285									
Asn	Pro	Phe	Cys	Asp	Arg	Cys	Val	Gln	Pro	Ala	Val	Phe	Ile	Ala	Leu						
						295					300										
Thr	Trp	Leu	Gly	Trp	Ile	Asn	Ser	Cys	Phe	Asn	Pro	Ile	Ile	Tyr	Ala						
305					310					315					320						
Phe	Asn	Lys	Glu	Phe	Arg	Lys	Val	Phe	Val	Lys	Met	Ile	Cys	Cys	His						

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          325                      330                      335
Lys Cys Arg Gly Val Thr Val Gly Pro Asn His Ala Asp Leu Asn Tyr
          340                      345                      350
Asp Pro Val Ala Met Arg Leu Lys Lys Arg Gly Glu Asn Ala Asn Gly
          355                      360                      365
Thr Val Asn Gly Asp Ala Asn Gly Lys Ala Asn Gly Asn Ile Glu Ala
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Gly Glu Gly Thr Ser Ser Ser
385                      390

<210> 5
<211> 463
<212> PRT
<213> FUGU RUBRIPES

<400> 5

Met Glu Asn Phe Tyr Asn Glu Thr Glu Pro Thr Glu Pro Arg Gly Gly
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Val Asp Pro Leu Arg Val Val Thr Ala Ala Glu Asp Val Pro Ala Pro
          20          25          30
Val Gly Gly Val Ser Val Arg Ala Leu Thr Gly Cys Val Leu Cys Ala
          35          40          45
Leu Ile Val Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val
          50          55          60
Ile Lys Phe Arg His Leu Arg Ser Lys Val Thr Asn Ala Phe Val Val
65          70          75          80
Ser Leu Ala Val Ser Asp Leu Phe Val Ala Val Leu Val Met Pro Trp
          85          90          95
Arg Ala Val Ser Glu Val Ala Gly Val Trp Leu Phe Gly Arg Phe Cys
          100          105          110
Asp Thr Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu
          115          120          125
Asn Leu Cys Val Ile Ser Met Asp Arg Tyr Trp Ala Ile Ser Asn Pro
          130          135          140
Phe Arg Tyr Glu Arg Arg Met Thr Arg Arg Phe Ala Phe Leu Met Ile
145          150          155          160
Ala Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln
          165          170          175
Leu Asn Trp His Arg Ala Asp Asn Asn Ser Ser Ala His Glu Gln Gly
          180          185          190

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Asp Cys Asn Ala Ser Leu Asn Arg Thr Tyr Ala Ile Ser Ser Ser Leu
 195 200 205
 Ile Ser Phe Tyr Ile Pro Val Leu Ile Met Val Gly Thr Tyr Thr Arg
 210 215 220
 Ile Phe Arg Ile Ala Gln Thr Gln Ile Arg Arg Ile Ser Ser Leu Glu
 225 230 235 240
 Arg Ala Ala Gly Gln Arg Ala Gln Asn Gln Ser His Arg Ala Ser Thr
 245 250 255
 His Asp Glu Ser Ala Leu Lys Thr Ser Phe Lys Arg Glu Thr Lys Val
 260 265 270
 Leu Lys Thr Leu Ser Val Ile Met Gly Val Phe Val Phe Cys Trp Leu
 275 280 285
 Pro Phe Phe Val Leu Asn Cys Val Val Pro Phe Cys Asp Val Asp Lys
 290 295 300
 Val Gly Glu Pro Pro Cys Val Ser Asp Thr Thr Phe Asn Ile Phe Val
 305 310 315 320
 Trp Phe Gly Trp Ala Asn Ser Ser Leu Asn Pro Val Ile Tyr Ala Phe
 325 330 335
 Asn Ala Asp Phe Arg Lys Ala Phe Thr Thr Ile Leu Gly Cys Ser Lys
 340 345 350
 Phe Cys Ser Ser Ser Ala Val Gln Ala Val Asp Phe Ser Asn Glu Leu
 355 360 365
 Val Ser Tyr His His Asp Thr Thr Leu Gln Lys Glu Pro Val Pro Gly
 370 375 380
 Pro Gly Ala His Arg Leu Val Ala Pro Leu Pro Gln Asn Arg Gly Asp
 385 390 395 400
 Ala Gly Pro Asn Phe Asp Lys Val Ser Val Val Ser Asp Asp Ser Arg
 405 410 415
 Ala Asp Arg Asn Leu Leu Leu Pro Ala Ile Leu Gln Cys Asp Cys Glu
 420 425 430
 Ala Glu Ile Ser Leu Asp Met Val Pro Phe Gly Ser Ser Gly Pro Ala
 435 440 445
 Asp Ser Phe Leu Ile Pro Gly Gln Ile Gln Asp Leu Gly Asp Leu
 450 455 460

<210> 6
 <211> 380
 <212> PRT
 <213> CYPRINUS CARPIO

<400> 6

Met Arg Ala Pro Arg Ser Gly Ala Gln His Ala Arg Pro Asn Arg Ala
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 Ala Leu Val Cys Ala Thr Val Val Arg Phe Arg His Leu Arg Ala Lys
 35 40 45
 Val Thr His Val Phe Ile Ala Ser Leu Ala Val Ser Asp Leu Leu Val
 50 55 60
 Ala Val Leu Val Met Pro Trp Lys Ala Val Ala Glu Val Ala Gly Phe
 65 70 75 80
 Trp Pro Phe Gly Ala Phe Cys Asn Ile Trp Val Ala Phe Asp Ile Met
 85 90 95
 Cys Ser Thr Ala Ser Ile Leu Asn Leu Cys Val Ile Ser Val Asp Arg
 100 105 110
 Tyr Trp Ala Ile Ser Ser Pro Phe Arg Tyr Glu Arg Lys Met Thr Pro
 115 120 125
 Arg Val Ser Phe Val Met Ile Gly Ala Ala Trp Thr Leu Ser Val Leu
 130 135 140
 Ile Ser Phe Ile Pro Val Gln Leu Asp Trp His Lys Thr Asp Ala Gly
 145 150 155 160
 Ala Ala Glu Pro Asn Ala Ser Asp Ala Asp Ser Cys Asp Ser Ser Leu
 165 170 175
 Ser Arg Val Tyr Ala Ile Ser Ser Ser Leu Ile Ser Phe Tyr Ile Pro
 180 185 190
 Val Ala Ile Met Ile Val Thr Tyr Thr Arg Ile Tyr Arg Ile Ala Gln
 195 200 205
 Val Gln Ile Arg Arg Ile Ala Ser Leu Glu Arg Ala Glu His Ala
 210 215 220
 Gln Ser Arg Arg Ser Asp Arg Ser Leu His Arg Ser Leu Lys Thr Ser
 225 230 235 240
 Phe Gln Arg Glu Thr Lys Val Leu Lys Thr Leu Ser Val Ile Ile Gly
 245 250 255
 Val Phe Val Cys Cys Trp Leu Pro Phe Phe Val Leu Asn Cys Val Val
 260 265 270
 Pro Phe Cys Arg Arg Glu Pro Cys Val Thr Asp Thr Thr Phe Asp Val
 275 280 285
 Phe Val Trp Phe Gly Trp Ser Asn Ser Ser Leu Asn Pro Val Ile Tyr
 290 295 300

Ala Phe Asn Ala Glu Phe Arg Arg Ala Phe Ser Ser Leu Leu Arg Cys
305 310 315 320

Arg Thr Pro Val Glu Thr Val Asn Ala Ser Asn Ala Leu Val Ser Tyr
325 330 335

Asn Arg Glu Ala Ala Ser Ala Cys Val Asn Ile Ile Pro Asn Val Val
340 345 350

Asp Glu Thr Leu Asp Arg Met Ser Gln Leu Ser Arg Gly Gly Asp Val
355 360 365

Asp Leu Asp Gly Ala Val His Ala Asn Gly Ile Leu
370 375 380

<210> 7

<211> 445

<212> PRT

<213> ANGUILLA ANGUILLA

<400> 7

Met Asp Leu Asn Phe Ser Thr Val Leu Asp Ser Gly Leu Ser Glu Thr
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Asp Ser Ser Val Arg Val Leu Thr Gly Cys Phe Leu Ser Ser Leu Ile
20 25 30

Val Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val Thr Lys
35 40 45

Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile Ser Leu
50 55 60

Ala Val Ser Asp Leu Leu Val Ala Ile Leu Val Met Pro Trp Lys Ala
65 70 75 80

Val Thr Glu Val Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys Asn Ile
85 90 95

Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu Asn Leu
100 105 110

Cys Ile Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro Phe Arg
115 120 125

Tyr Glu Arg Lys Met Thr Pro Lys Val Ala Phe Val Met Ile Ser Val
130 135 140

Ala Trp Thr Leu Ser Leu Leu Ile Ser Phe Ile Pro Val Gln Leu Asn
145 150 155 160

Trp His Lys Ala Gln Thr Thr Ser Tyr Phe Asp His Asn Gly Ser Tyr
165 170 175

Gly Asp Leu Leu Leu Asp Asn Cys Asp Ser Ser Leu Asn Arg Thr Tyr

	180						185						190					
Ala	Ile	Ser	Ser	Ser	Leu	Ile	Ser	Phe	Tyr	Ile	Pro	Val	Ala	Ile	Met			
		195					200					205						
Ile	Val	Thr	Tyr	Thr	Arg	Ile	Tyr	Arg	Ile	Ala	Gln	Lys	Gln	Ile	Arg			
		210					215				220							
Arg	Ile	Ser	Ala	Leu	Glu	Arg	Ala	Ala	Glu	Ser	Ala	Lys	Asn	Arg	His			
					230					235					240			
Asn	Ser	Met	Gly	Asn	Ser	Ser	Ser	Val	Glu	Thr	Glu	Ser	Ser	Phe	Lys			
				245					250					255				
Met	Ser	Phe	Lys	Arg	Glu	Thr	Lys	Val	Leu	Lys	Thr	Leu	Ser	Val	Ile			
			260					265					270					
Met	Gly	Val	Phe	Val	Cys	Cys	Trp	Leu	Pro	Phe	Phe	Ile	Leu	Asn	Cys			
		275					280					285						
Met	Val	Pro	Phe	Cys	Glu	Gln	Ala	His	Pro	Asn	Gly	Ser	Ala	Asp	Phe			
		290				295					300							
Pro	Cys	Val	Ser	Ser	Thr	Thr	Phe	Asn	Val	Phe	Val	Trp	Phe	Gly	Trp			
					310					315					320			
Ala	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Asn	Ala	Asp	Phe			
				325					330					335				
Arg	Lys	Ala	Phe	Ser	Ile	Leu	Leu	Gly	Cys	His	Arg	Leu	Cys	Pro	Gly			
			340					345					350					
Ser	Asn	Ala	Ile	Glu	Ile	Val	Ser	Ile	Asn	Asn	Asn	Gly	Ala	Pro	Pro			
		355					360					365						
Gln	Leu	Val	His	Asn	Gln	Pro	Lys	Ala	Cys	Phe	Ser	Lys	Gly	Cys	Ile			
		370				375					380							
Pro	Lys	Glu	Gly	Asn	Leu	Arg	His	Gly	Ile	Pro	His	Thr	Ile	Leu	Ser			
					390					395					400			
Gln	Asp	Glu	Glu	Leu	Gln	Lys	Lys	Gly	Asn	Ala	Ile	Glu	Arg	Ile	Ser			
				405					410					415				
Pro	Ala	Leu	Ser	Gly	Ser	Leu	Asp	Ser	Glu	Ala	Asp	Leu	Ser	Leu	Asp			
			420					425					430					
Lys	Ile	Asn	Pro	Thr	Thr	Gln	Asn	Gly	Gln	Asn	Ser	Thr						
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<210>      8
<211>     428
<212>     PRT
<213>     MELEAGRIS GALLOPAVO
<400>      8
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Met Thr Pro Leu Pro Ala Gly Asn Gly Ser Val Pro Asn Cys Ser Trp
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Ala Ala Val Leu Ser Arg Gln Trp Ala Val Gly Ala Ala Leu Ser Ile
20      25      30

Thr Ile Leu Val Ile Val Ala Gly Asn Leu Leu Val Ile Val Ala Ile
35      40      45

Ala Lys Thr Pro Arg Leu Gln Thr Met Thr Asn Val Phe Val Thr Ser
50      55      60

Leu Ala Cys Ala Asp Leu Val Met Gly Leu Leu Val Val Pro Pro Gly
65      70      75

Ala Thr Ile Leu Leu Ser Gly His Trp Pro Tyr Gly Thr Val Val Cys
85      90      95

Glu Leu Trp Thr Ser Leu Asp Val Leu Cys Val Thr Ala Ser Ile Glu
100     105     110

Thr Leu Cys Ala Ile Ala Val Asp Arg Tyr Leu Ala Ile Thr Ala Pro
115     120     125

Leu Gln Tyr Glu Ala Leu Val Thr Lys Gly Arg Ala Trp Ala Val Val
130     135     140

Cys Met Val Trp Ala Ile Ser Ala Phe Ile Ser Phe Leu Pro Ile Met
145     150     155     160

Asn His Trp Trp Arg Asp Gly Ala Asp Glu Gln Ala Val Arg Cys Tyr
165     170     175

Asp Asp Pro Arg Cys Cys Asp Phe Val Thr Asn Met Thr Tyr Ala Ile
180     185     190

Val Ser Ser Thr Val Ser Phe Tyr Val Pro Leu Leu Val Met Ile Phe
195     200     205

Val Tyr Val Arg Val Phe Ala Val Ala Thr Arg His Val Gln Leu Ile
210     215     220

Gly Lys Asp Lys Val Arg Phe Leu Gln Glu Asn Pro Ser Leu Ser Ser
225     230     235     240

Arg Gly Gly Arg Trp Arg Arg Pro Ser Arg Leu Leu Ala Ile Lys Glu
245     250     255

His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu
260     265     270

Cys Trp Leu Pro Phe Phe Val Ala Asn Ile Ile Lys Val Phe Cys Arg
275     280     285

Pro Leu Val Pro Asp Gln Leu Phe Leu Phe Leu Asn Trp Leu Gly Tyr
290     295     300

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Val Asn Ser Ala Phe Asn Pro Ile Ile Tyr Cys Arg Ser Pro Asp Phe
305 310 315 320

Arg Ser Ala Phe Arg Lys Leu Leu Cys Cys Pro Arg Arg Ala Asp Arg
325 330 335

Arg Leu His Ala Ala Pro Gln Asp Pro Gln His Cys Ser Cys Ala Phe
340 345 350

Ser Pro Arg Gly Asp Pro Met Glu Asp Ser Lys Ala Val Asp Pro Gly
355 360 365

His Leu Arg Glu Asp Ser Glu Val Gln Gly Ser Gly Arg Arg Glu Glu
370 375 380

Asn Ala Ser Ser His Gly Gly Gly His Gln Gln Arg Pro Leu Gly Glu
385 390 395 400

Cys Trp Leu Gln Gly Met Gln Ser Met Leu Cys Glu Gln Leu Asp Glu
405 410 415

Phe Thr Ser Thr Glu Met Pro Ala Gly Pro Ser Val
420 425

<210> 9

<211> 418

<212> PRT

<213> MUS MUSCULUS

<400> 9

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Ser Arg Ala Pro Asp His Asp Val Thr Gln Glu Arg Asp Glu Ala Trp
20 25 30

Val Val Gly Met Ala Ile Leu Met Ser Val Ile Val Leu Ala Ile Val
35 40 45

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50 55 60

Gln Thr Val Thr Asn Tyr Phe Ile Ile Ser Leu Ala Cys Ala Asp Leu
65 70 75 80

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ser His Ile Leu Met
85 90 95

Lys Met Trp Asn Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100 105 110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
115 120 125

Val Asp Arg Tyr Val Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
130 135 140

Leu Thr Lys Asn Lys Ala Arg Val Val Ile Leu Met Val Trp Ile Val
 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
 165 170 175
 Thr His Lys Lys Ala Ile Asp Cys Tyr Thr Glu Glu Thr Cys Cys Asp
 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
 195 200 205
 Tyr Val Pro Leu Cys Val Met Val Phe Val Tyr Ser Arg Val Phe Gln
 210 215 220
 Val Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
 225 230 235 240
 His Ala Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Ser Gly His
 245 250 255
 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
 275 280 285
 Phe Phe Ile Val Asn Ile Val His Val Ile Arg Asp Asn Leu Ile Pro
 290 295 300
 Lys Glu Val Tyr Ile Leu Leu Asn Trp Leu Gly Tyr Val Asn Ser Ala
 305 310 315 320
 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
 325 330 335
 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Ser Lys Thr Tyr Gly Asn
 340 345 350
 Gly Tyr Ser Ser Asn Ser Asn Gly Arg Thr Asp Tyr Thr Gly Glu Pro
 355 360 365
 Asn Thr Cys Gln Leu Gly Gln Glu Arg Glu Gln Glu Leu Leu Cys Glu
 370 375 380
 Asp Pro Pro Gly Met Glu Gly Phe Val Asn Cys Gln Gly Thr Val Pro
 385 390 395 400
 Ser Leu Ser Val Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser
 405 410 415
 Pro Leu

<210> 10
 <211> 418

<212> PRT
 <213> SUS SCROFA

<400> 10

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Met Gly Gln Pro Gly Asn Arg Ser Val Phe Leu Leu Ala Pro Asn Gly
1          5          10          15

Ser His Ala Pro Asp Gln Asp Val Pro Gln Glu Arg Asp Glu Ala Trp
20        25        30

Val Val Gly Met Ala Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
35        40        45

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50        55        60

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
65        70        75        80

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ser His Ile Leu Met
85        90        95

Lys Met Trp Thr Phe Gly Ser Phe Trp Cys Glu Phe Trp Ile Ser Ile
100       105       110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
115       120       125

Val Asp Arg Tyr Leu Ala Ile Thr Ser Pro Phe Lys Tyr Gln Cys Leu
130       135       140

Leu Thr Lys Asn Lys Ala Arg Val Val Ile Leu Met Val Trp Val Val
145       150       155       160

Ser Gly Leu Ile Ser Phe Leu Pro Ile Lys Met His Trp Tyr Gln Ala
165       170       175

Thr His Arg Glu Ala Leu Asn Cys Tyr Ala Glu Glu Ala Cys Cys Asp
180       185       190

Phe Phe Thr Asn Gln Pro Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
195       200       205

Tyr Leu Pro Leu Val Val Met Val Phe Val Tyr Ser Arg Val Phe Gln
210       215       220

Val Ala Arg Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
225       230       235       240

His Ala Gln Asn Leu Ser Gln Ala Glu Gln Asp Gly Arg Ser Gly Pro
245       250       255

Gly His Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
260       265       270

Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

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275	280	285
Phe Phe Ile Val Asn Ile Val His Gly Ile His Asp Asn Leu Ile Pro		
290	295	300
Lys Glu Val Tyr Ile Leu Leu Asn Trp Val Gly Tyr Val Asn Ser Ala		
305	310	315
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Met Ala Phe		
325	330	335
Gln Glu Leu Leu Cys Leu His Arg Ser Ser Leu Lys Ala Tyr Gly Asn		
340	345	350
Gly Cys Ser Ser Asn Ser Asn Gly Arg Thr Asp Tyr Thr Gly Glu Gln		
355	360	365
Ser Gly Cys Tyr Leu Gly Glu Glu Lys Asp Ser Glu Arg Leu Cys Glu		
370	375	380
Asp Ala Pro Gly Pro Glu Gly Cys Ala His Arg Gln Gly Thr Val Pro		
385	390	395
Asp Asp Ser Thr Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser		
405	410	415

Met Leu

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 <212> PRT
 <213> CANIS FAMILIARIS

<400> 11

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20	25 30
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35	40 45
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Arg Phe Glu Arg Leu	
50	55 60
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65	70 75 80
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ser His Ile Leu Met	
85	90 95
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100	105 110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
 115 120 125
 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
 130 135 140
 Leu Thr Lys Asn Lys Ala Arg Val Val Ile Leu Met Val Trp Ile Val
 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
 165 170 175
 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Lys Glu Thr Cys Cys Asp
 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
 195 200 205
 Tyr Leu Pro Leu Val Val Met Val Phe Val Tyr Ser Arg Val Phe Gln
 210 215 220
 Val Ala Gln Arg Gln Leu Gln Lys Ile Asp Arg Ser Glu Gly Arg Phe
 225 230 235 240
 His Ala Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Ser Gly His
 245 250 255
 Gly His Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
 275 280 285
 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Pro
 290 295 300
 Lys Glu Val Tyr Ile Leu Leu Asn Trp Val Gly Tyr Val Asn Ser Ala
 305 310 315 320
 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
 325 330 335
 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn
 340 345 350
 Gly Tyr Ser Asn Asn Ser Asn Ser Arg Ser Asp Tyr Ala Gly Glu His
 355 360 365
 Ser Gly Cys His Leu Gly Gln Glu Lys Asp Ser Glu Leu Leu Cys Glu
 370 375 380
 Asp Pro Pro Gly Thr Glu Asp Arg Gln Gly Thr Val Pro Ser Asp Ser
 385 390 395 400
 Val Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 405 410 415

<210> 12
 <211> 28
 <212> PRT
 <213> HOMO SAPIENS

<400> 12

Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser Leu Ile Ile Ala
 1 5 10 15

Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 20 25

<210> 13
 <211> 21
 <212> PRT
 <213> HOMO SAPIENS

<400> 13

Phe Thr Leu Asn Leu Ala Val Ala Asp Thr Leu Ile Gly Val Ala Ile
 1 5 10 15

Ser Gly Leu Leu Thr
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<210> 14
 <211> 19
 <212> PRT
 <213> HOMO SAPIENS

<400> 14

Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val Met Leu
 1 5 10 15

Ile Thr Phe

<210> 15
 <211> 28
 <212> PRT
 <213> HOMO SAPIENS

<400> 15

Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly Leu Trp Leu
 1 5 10 15

Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile
 20 25

<210> 16
 <211> 21
 <212> PRT
 <213> HOMO SAPIENS

<400> 16

Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro Ala Met Leu Leu
 1 5 10 15

Phe Val Phe Phe Tyr
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<210> 17

<211> 22

<212> PRT

<213> HOMO SAPIENS

<400> 17

Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro Phe
 1 5 10 15

Leu Ile Thr Gly Ile Val
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<210> 18

<211> 20

<212> PRT

<213> HOMO SAPIENS

<400> 18

Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser Leu Leu Asn Pro Leu Ile
 1 5 10 15

Tyr Ala Tyr Trp
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<210> 19

<211> 840

<212> DNA

<213> homo sapiens

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 gctgtggctg acaccttgat tgggtgtggc atctctggcc tactcacaga ccagctctcc 180
 agcccttctc ggccacaca gaagaccctg tgcagcctgc ggtatggcatt tgtcacttcc 240
 tccgcagctg cctctgtcct caccgtcatg ctgatcacct ttgacaggta ccttgccatc 300
 aagcagccct tccgtactt gaagatcatg agtgggttcg tggccggggc ctgcattgcc 360
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 cagactgcct acaaaggcca gtgcagcttc ttgtctgtat ttcacctca cttcgtgctg 480
 accctctcct gcgttggctt ctcccagcc atgtctctct ttgtcttctt ctactgcgac 540

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atgctcaaga ttgctccat gcacagccag cagattcgaa agatggaaca tgcaggagcc 600
atggctggag gttatcgatc cccacggact cccagcgact tcaaagctct ccgtactgtg 660
tctgtttcca ttgggagctt tgctctatcc tggacccctc tcttatacac tggcattgtg 720
cagggtggct gccaggagtg tcacctctac ctagtgtgg aacggtaect gtggctgtgc 780
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<210> 21
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<400> 21
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<400> 22
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<210> 23
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<400> 23

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Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
1          5          10

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<400> 24

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Gln Lys Thr Leu Cys Ser Leu Arg Met Ala Phe Val Thr
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<210> 25
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 <213> HOMO SAPIENS

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Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe
 1 5 10

<210> 26
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 <212> PRT
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Phe Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu
 1 5 10

<210> 27
 <211> 27
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<400> 27

Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val Met Leu Ile Thr Phe
 1 5 10 15

Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 20 25

<210> 28
 <211> 26
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 <213> HOMO SAPIENS

<400> 28

Phe Leu Pro Leu Gly Ile Pro Met Phe Gln Gln Thr Ala Tyr Lys Gly
 1 5 10 15

Gln Cys Ser Phe Phe Ala Val Phe His Pro
 20 25

<210> 29
 <211> 16
 <212> PRT
 <213> HOMO SAPIENS

<400> 29

Ile Val Gln Val Ala Cys Gln Glu Cys His Leu Tyr Leu Val Leu Glu
 1 5 10 15

<210> 30
 <211> 38
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 <213> HOMO SAPIENS

<400> 30

Gly Cys Ala Gly Cys Ala Gly Cys Gly Gly Cys Cys Gly Cys Gly Cys
 1 5 10 15

Cys Thr Cys Cys Cys Thr Cys Ala Thr Cys Ala Thr Thr Gly Cys Thr
 20 25 30

Ala Cys Thr Ala Ala Cys
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<210> 31
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 <213> HOMO SAPIENS

<400> 31

Gly Cys Ala Gly Cys Ala Gly Thr Cys Gly Ala Cys Gly Cys Cys Ala
 1 5 10 15

Thr Cys Ala Ala Ala Cys Thr Cys Thr Gly Ala Gly Cys Thr Gly Gly
 20 25 30

Ala Gly Ala Thr Ala Gly
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<210> 32
 <211> 39
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 <213> HOMO SAPIENS

<400> 32

Gly Cys Ala Gly Cys Ala Gly Cys Gly Gly Cys Cys Gly Cys Ala Thr
 1 5 10 15

Gly Gly Ala Ala Thr Cys Ala Thr Cys Thr Thr Thr Cys Thr Cys Ala
 20 25 30

Thr Thr Thr Gly Gly Ala Gly
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<210> 33
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 <213> HOMO SAPIENS

<400> 33

Gly Cys Ala Gly Cys Ala Gly Thr Cys Gly Ala Cys Gly Cys Cys Ala
 1 5 10 15

Gly Thr Gly Ala Thr Ala Ala Gly Gly Ala Ala Gly Gly Gly Gly Gly
 20 25 30

Thr Cys Cys Ala Gly
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<210> 34
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 <212> PRT
 <213> bacteriophage T7

<400> 34

Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 35
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 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
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<400> 37
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<210> 38
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 <213> Homo sapiens

<400> 38
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<400> 42
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<400> 47
tgaggagacg gtgaccaggg tgcc                24

<210> 48
<211> 24
<212> DNA
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<400> 48
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<210> 49

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<400> 50
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<210> 51
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 <210> 68

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<400> 69
acgtttaatc tccagtcgtg tccc                24

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<400> 70
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<210> 71
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cagtcctgcc tgactcagcc tgc                23

<210> 72
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<400> 72
tcctatgtgc tgactcagcc acc                23

<210> 73
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<400> 73
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<210> 74
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<400> 74
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<210> 75
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caggctgtgc tcactcagcc gtc

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<210> 76
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23